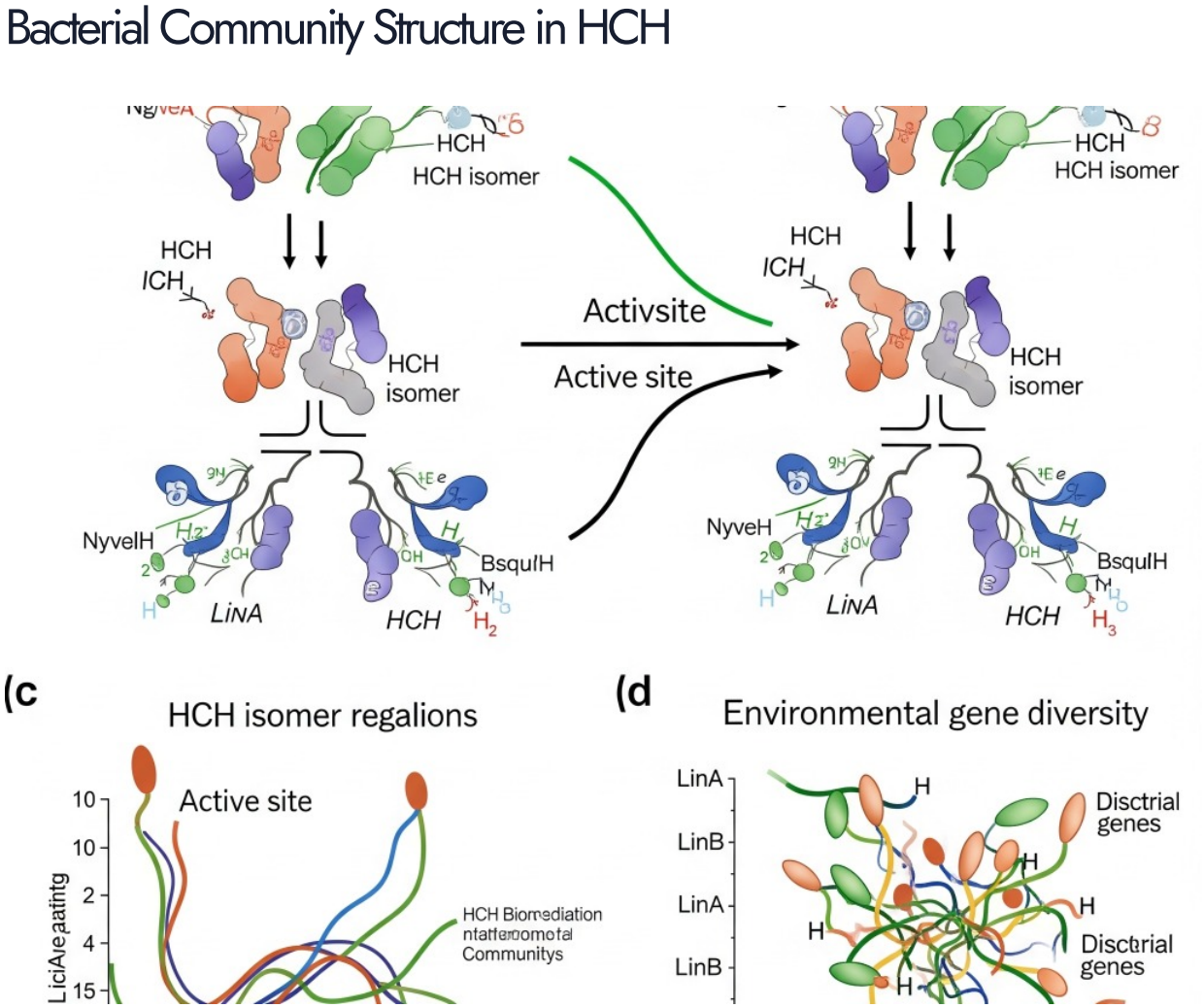

Bacterial Community Structure in HCH Contaminated Pond Soil Near Lindane Manufacturing Unit

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Introduction

An introduction to the topic "Bacterial Community Structure in HCH" The presence of hazardous organochlorine compounds in soil and water bodies poses significant environmental and public health challenges. Among them, hexachlorocyclohexane (HCH) and its isomers, byproducts of lindane production, have been found to persist in the environment due to their chemical stability.

This study investigates the impact of HCH contamination on microbial community structure in pond soil adjacent to a lindane manufacturing facility in Lucknow, India. Understanding the bacterial diversity in such environments not only helps assess the extent of contamination but also identifies potential microorganisms involved in bioremediation.

This article will benefit microbiologists, environmental scientists, soil ecologists, and policy-makers concerned with environmental safety, pollution control, and restoration of contaminated lands. The focus keyword, *HCH-contaminated pond soil*, appears early to ensure optimal SEO placement.

Microbial Diversity and Residue Analysis in HCH-Contaminated Pond Soil

"3. RESULTS

3.1. Site for soil collection

Site was selected with a heavy load of pesticide waste (HCH muck) discarded by the HCH manufacturing industry. The site is located near India Pesticides Limited (IPL), Chinhat, Lucknow. IPL (26° 55′ N and 81° 3′ E) is situated 25 km north-east of the Lucknow railway station (26° 52′ N and 81° 1′ E).

Since 1997, IPL has been involved in the production of lindane and in the present time it is the only lindane production plant operating in India. As already described, lindane is produced by purification of technical HCH. As a result of purification, HCH muck consisting of waste isomers has

been dumped by the side of the site.

The waste HCH isomers left after lindane purification have been stored temporarily in the muck yard behind the factory (Fig. 2.4). The water flowing from the backyard of this factory accumulates in a nearby pond area.

Soil and water samples were collected from pond water and soil sediments (26° 54′ N and 81° 4′ E). HCH residue levels and microbial diversity was examined in both soil and water samples.

Evaluation of HCH Residues

3.2. Evaluation of HCH residues from pond soil and water sample
Result of residue analysis from soil and water samples is shown in Table 2.2 and 2.3. The HCH concentration was found to be 4.8 mg kg^{-1} of soil and 18 mg l^{-1} of water.

Interestingly pond soil and water samples contained α- and β- HCH at remarkably varied concentrations. In the pond soil high proportions of β-HCH can be due to faster degradation of α-HCH as compared to the persistent β-HCH.

The water sample contained 18 mg l^{-1} Σ-HCH, the α-HCH predominated in this sample, possibly as a result of preferential solubility of this isomer.

Table 2.2: Residue analyses of soil samples collected from pond soil.
(Values are mean of three replicates.)

Sample	α	β	γ	δ	ε	Σ-HCH
PS1	0.01	5.22	0.01	0.02	0.21	5.47
PS2	0.44	8.25	0.01	0.02	0.30	9.02
PS3	0.01	3.04	0.00	0.01	0.15	3.21
PS4	0.01	1.49	0.01	0.01	0.09	1.61

Table 2.3: Residue analyses of water samples collected from pond water.

Sample	α	β	γ	δ	ε	Σ-HCH
PW1	15.4	5.9	0.3	ND	ND	21.3
PW2	10.7	4.2	ND	ND	ND	14.9

ND: Not detected

DNA Extraction and Genetic Diversity

3.3. Soil DNA extraction from HCH contaminated pond soil and water samples

The four soil samples were pooled into two each and water as one sample. Soil DNA was extracted and quantitated using agarose gel electrophoresis (Fig. 2.5).

DNA concentrations of soil and water sample were different. Water DNA yield was much less as compared to soil DNA samples.

3.4. Ecological diversity indices and rarefaction analysis

Bacterial diversity indices were calculated to study the distribution and diversity in pond soil and water sample contaminated with HCH (Table 2.4).

A low value was seen for Simpson's diversity index, this site was not diverse due to high amount of contamination. Equitability Index suggests evenness in the samples and Dominance Index indicates that the samples were not dominated by a particular species.

The Chao1 estimator predictions and Shannon-Wiener index were low for pond water diversity whereas a relatively higher value was observed in soil sample.

Table 2.4: Standard ecological estimates of diversity for pond soil and water.

Sample	Chao1	Shannon	Simpson	Dominance	Equitability
Pond soil	94.60	3.3758	0.02897	0.971	0.9349

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Pond water    52.00    2.6654    0.03463    0.966
0.9613
```

Microbial Community Composition

3.5. Microbial diversity at pond soil and water sample

Thirty seven different genera were covered by 16S rRNA gene clone library of pond soil. Taxonomic affiliations of 16S rRNA gene sequences were obtained using SeqMatch tool of the Ribosomal Database Project (RDP) release 10.

The obtained gene sequences showed similarity either with the uncultured or cultured bacterial population.

Among these, majority of the clone sequences in the soil sample belonged to Gemmatimonas, Thiobacillus followed by Sphingomonas, Sphingobium, Steriodobacter. All the genera can be divided into 16 phyla. From the clones analyzed in the samples, the majority corresponded to Proteobacteria, followed by Gemmatimonadetes and Acidobacteria.

The diversity of the pond water was different from the soil sample. Out of all the bacterial 16S rRNA gene sequences, 7 different phyla were identified, Proteobacteria (43%) and Actinobacteria (28%) were the most representative groups. Among Proteobacteria, any representatives of γ and δ Proteobacteria were not observed.

Phospholipids Fatty Acid Analysis (PLFA)

3.6. Microbial diversity –Phospholipids fatty acid analysis (PLFA)

The microbial community structure of the present study area, as suggested by the PLFA profiles, showed high percentages of fatty acids that are characteristic of bacterial community. A total of 11 types of fatty acids in the range of C14 to C18 were determined. They consisted of saturated fatty acids, branched fatty acids.

The percentage abundance for Gram positive and Gram negative were 18.3% and 57% respectively. The ratio for Gram (+)/Gram (-) was found to be 3.2. The lack of 10me18:0 and 12me18:0 in the pond soil suggests that actinomycetes were of minor importance in these soils.

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